WORKBOOK

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Rhys Lewis

SACE STAGE 2
Australian Curriculum

Biology

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249 Henley Beach Road, Torrensville SA 5031 AUSTRALIA
Telephone: +61 8 8354 0006
Fax: +61 8 8354 0008
Email: office@sasta.asn.au
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Sections added to extend the understanding of the reader
The following information has been added to further the understanding of the reader. The author and SASTA acknowledge that this information is not assessable criteria as per the SACE subject outline for stage 2 biology in 2018.

The choice to read the information and complete the questions provided rests with the reader.
Fibrous and globular proteins (p28); Effect of substrate and product concentration on the rate of enzyme-catalysed reactions (p36); Reversible and irreversible inhibitors (p37 and 38); Question 14 (e) (p45); Chromatin remodelling (p49 and 50); Non-coding RNA (p50); Question 18 (c) (p54); Question 19 (second dot-point only) (p55); The names of the different types of mutations (missense, silent, nonsense); (p56 and 57); The names of the different chromosomal mutations (p58); Question 20 (a) (p62); Question 21 (d) (p63); Southern blotting (p72); Explanation of the process of DNA sequencing (p73); The production of electropherograms from a DNA sample (p74); Question 26 (c) part (1) (p76); Identifying host cells using antibiotic resistance genes (p91 and 92); Fimbriae (prokaryote structure) (p116); Question 36 (d) (p121); Anabolic and catabolic reactions (p125); Question 40 (g) and (h) (p145); Regulatory enzymes (p162); Question 47 (e) (2) (p166); Cytokinesis in animal and plant cells (p174); Question 50 (c) (p176); Question 53 (d) parts (1) and (2) (p189); Role of cyclins B and E (p198); Metastasis (cancer) (p199); Malignant and benign tumours (p199); Question 57 (c) (p200); Question 58 (a) (p202); Osmoconformers and osmoregulators (p229); Question 64 (b) and (c) (p232); Question 65 (d) (2) (p234); Question 72 (e) part (2) (p259); Question 74 (c), (d) and (f) (p263); Gluconeogenesis (p266); Use of basal and bolus insulin in treatment of diabetes (p268); Question 75 (f) (p270); Question 77 (f) (p274); Hypothyroidism and hyperthyroidism (p275); Question 78 (b) (p276); The role of renin and angiotensin in the regulation of blood pressure (p282); Hypotension and hypertension (p282); Question 94 (a) part (1) (p333); Question 94 (b) part (4) (p334).

Contents

1.2: Structure and function of proteins

A gene consists of a unique sequence of nucleotides that code for a protein or RNA molecule.

- Distinguish between exons and introns as coding and non-coding segments of DNA found in genes.
- Describe how both exons and introns are transcribed but only the information contained in exons is translated to form a polypeptide.

A **gene** is a length of DNA which codes for the assembly of a protein or RNA molecule. A single gene contains hundreds to millions of bases. Chromosomes contain hundreds to thousands of different genes. Genes in eukaryotes contain segments that code for a protein as well as non-coding segments.

- **Exons** are segments of a gene that code for the synthesis of a protein.
- **Introns** are segments of a gene that do not code for the synthesis of a protein.

Protein synthesis occurs in two stages in cells.

Stage	Description
1. Transcription	The genetic code is copied from the gene (DNA) to messenger RNA (mRNA).
2. Translation	The protein molecule is assembled using the genetic code on the mRNA.

In transcription, the entire gene (exons and introns) is copied into a messenger RNA (mRNA) molecule. The mRNA molecule synthesised in transcription is called **pre-mRNA** as it is premature and is modified before translation occurs. Pre-mRNA is modified in a process called **RNA splicing**.

RNA splicing

RNA splicing is the process of removing introns from pre-mRNA forming **mature-mRNA** that contains only exons. The process of splicing is carried out by a protein-RNA complex called a **spliceosome** (Figure 1.10). Spliceosomes remove different introns from a pre-mRNA molecule forming a range of different **mature mRNAs** that are translated into a variety of different proteins.

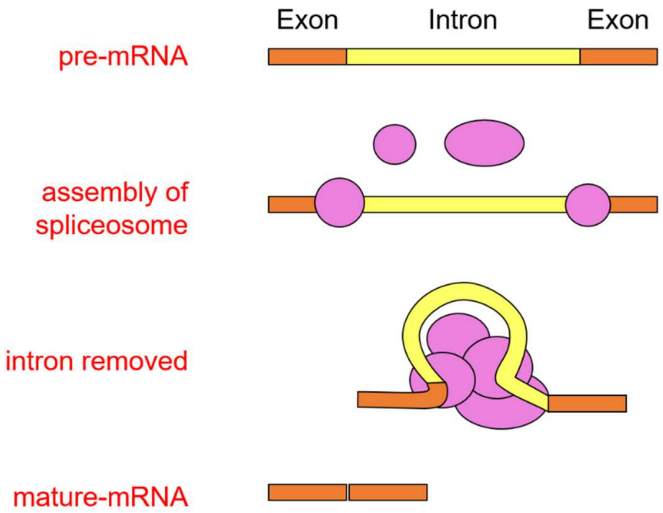


Figure 1.10: Removal of introns from pre-mRNA.

Question 7

Broad spectrum antibiotics are effective against a wide range of microorganisms.

Chloramphenicol and tetracycline are broad spectrum antibiotics that act on ribosomes in bacteria.

(a) State the location of ribosomes in a prokaryotic cell such as a bacterium.

_____ (1 mark) **KA1**

(b) Chloramphenicol binds to the bacterial ribosome and inhibits the formation of bonds between amino acids.

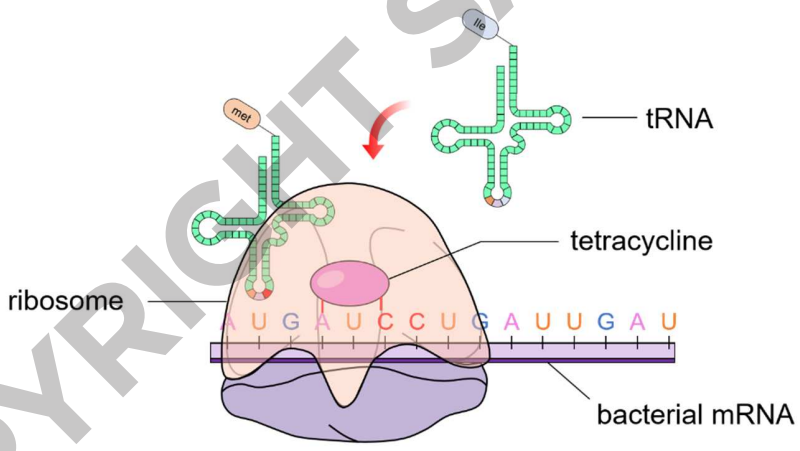
Explain how the action of chloramphenicol leads to the death of bacteria.

_____

_____

_____ (2 marks) **KA2**

(c) Tetracycline also binds to the bacterial ribosome as shown in the diagram below.



Use the information in the diagram to describe how tetracycline inhibits the synthesis of proteins in bacteria.

_____

_____

_____

_____ (3 marks) **KA2**

(d) Use the information in the question to state why both chloramphenicol and tetracycline are categorised as broad-spectrum antibiotics.

_____

_____ (1 mark) **KA2**

Proteins are essential to cell structure and function.

Examples of proteins with specific shapes include enzymes, some hormones, receptor proteins, and antibodies.

- Explain why the three-dimensional structure of a protein is critical to its function.

The three-dimensional structure of a protein determines its biological function in a cell. Proteins carry out functions by interacting with other molecules in a cell. The three-dimensional structure of a protein creates one or more regions that interact with other molecules or ions in a cell. In many cases, the shape of the protein molecule is **complementary** to the shape of its target molecule or ion, meaning that the two molecules interact with high specificity.

Example 1: Enzymes

Enzymes are protein catalysts that increase the rate of chemical reactions in cells by binding to target molecules called substrates. The shape of an enzyme is complementary to the shape of its substrate which facilitates binding between the two molecules (Figure 1.19).

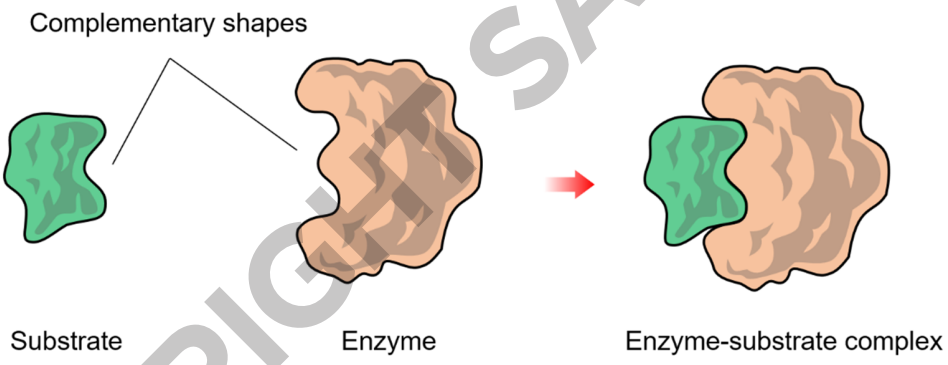


Figure 1.19: Enzyme-substrate interaction.

Example 2: Peptide hormones

Hormones regulate physiology and behaviour in a multicellular organism by facilitating communication between cells. Hormones are released from endocrine glands and travel to target cells via the circulatory system. Examples of peptide hormones include insulin, glucagon, and anti-diuretic hormone (ADH).

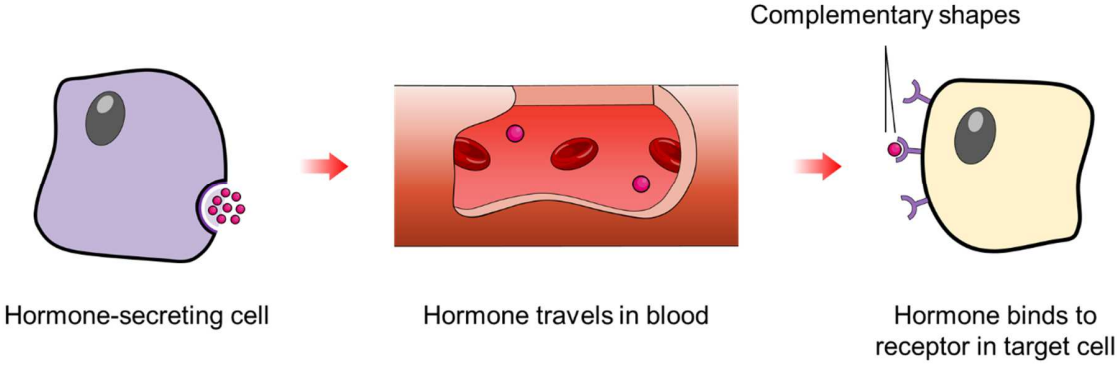
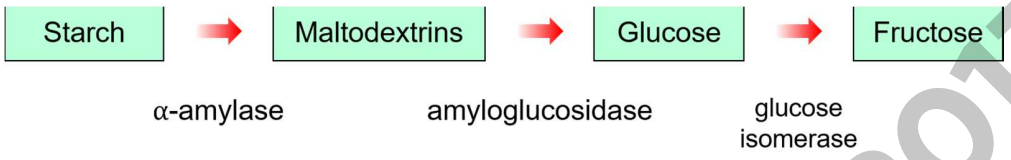


Figure 1.20: Hormone secretion and binding.

Question 11

High fructose corn syrup is used as a sweetener in soft drinks and confectionery.

Corn starch (raw material) is converted to fructose in three stages; each involves the use of an enzyme.



(a) State the function of enzymes in chemical reactions.

_____ (1 mark) **KA1**

(b) State the name of the substrate for amyloglucosidase enzyme.

_____ (1 mark) **KA1**

(c) Describe the induced-fit model of enzyme substrate binding using glucose (substrate) and glucose isomerase (enzyme) as an example.

_____

_____

_____

_____ (2 marks) **KA1**

(d) State why each enzyme catalyses only one reaction in the conversion of starch to fructose.

_____

_____

_____ (1 mark) **KA1**

(e) The conversion of starch to high fructose corn syrup (HFCS) is carried out on an industrial scale to provide HFCS for the food and beverage industry.

Research is being conducted to find versions of the enzymes above that are stable at higher temperatures.

Explain the benefit to manufacturers of HFCS in using enzymes that are stable at higher temperatures.

_____

_____

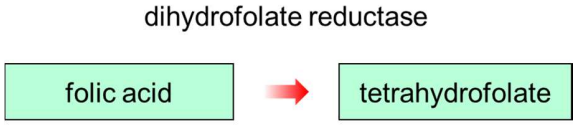
_____

_____ (2 marks) **KA2**

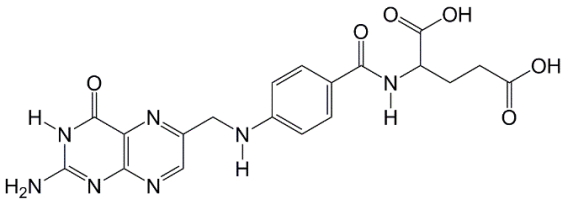
Question 14

Methotrexate is a drug that is used to treat various forms of cancer.

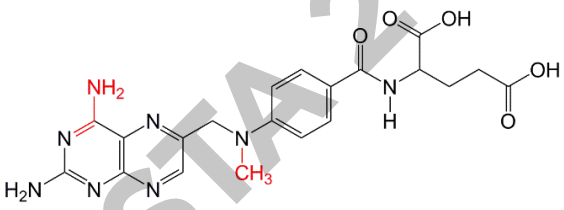
Methotrexate is an inhibitor of dihydrofolate reductase (DHFR), an enzyme that converts folic acid to tetrahydrofolate.



The chemical structures of folic acid and methotrexate are shown below.



folic acid



methotrexate

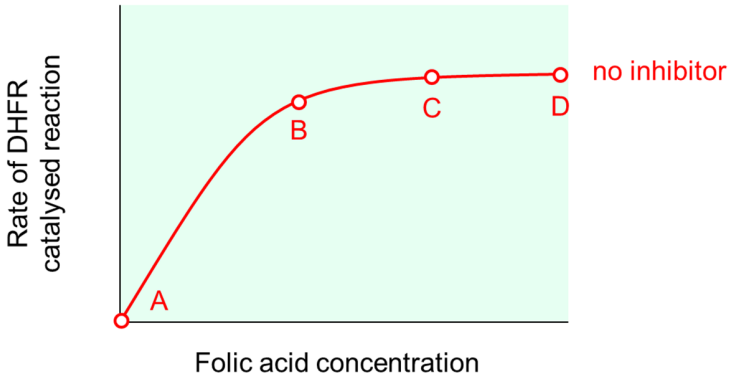
(a) State and explain whether methotrexate is a competitive or non-competitive inhibitor of DHFR.

(2 marks) **KA2**

(b) Explain how methotrexate inhibits the biological function of DHFR.

(2 marks) **KA1**

(c) The graph below shows the effect of folic acid (substrate) concentration on the rate of the DHFR-catalysed reaction.



(1) Explain the shape of the curve between points A and B on the graph.

(2 marks) **KA1**

(2) Explain the shape of the curve between points C and D on the curve.

(2 marks) **KA1**

(3) Sketch a curve on the graph below to show the rate of the DHFR-catalysed reaction in the presence of methotrexate.

(1 mark) **KA4**

(d) Tetrahydrofolate is a coenzyme for the enzyme thymidylate synthetase (TS).

TS is involved in the synthesis of thymine nucleotides which are needed for DNA synthesis.

Explain how methotrexate (anti-cancer drug) prevents cancer cells from dividing.

(4 marks) **KA2**

(e) Adrucil is another medication used to treat cancer.

Adrucil is an irreversible inhibitor of thymidylate synthetase (TS).

State the difference between the action of reversible and irreversible enzyme inhibitors.

(1 mark) **KA1**

(f) State why cancer sufferers taking adrucil and methotrexate experience a range of side effects.

(1 mark) **KA3**

There are several mechanisms by which genes are turned on or off in cells. Genes that are turned off are described as being **silenced**. Silencing genes involves adding or removing chemical groups from DNA or the histone proteins associated with DNA (in chromatin) in eukaryotes.

DNA methylation

Genes can be switched on and off by the addition or removal of methyl groups ($-CH_3$) from the DNA molecules in cells. Methyl groups are added and removed from cytosine (C) nucleotides in cells by enzymes called DNA methyltransferases (DNMTs). The addition (methylation) and removal (demethylation) of a methyl group to cytosine nucleotides in DNA is shown in Figure 1.33.

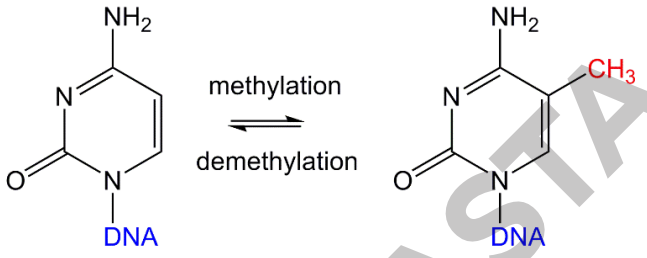


Figure 1.33: DNA methylation/demethylation of the cytosine nucleotide.

Adding a methyl group to cytosine nucleotides in a gene inhibits the action of RNA polymerase, which prevents transcription of DNA and effectively silences a gene. Removal of a methyl group from cytosine nucleotides allows transcription to occur (Figure 1.34).

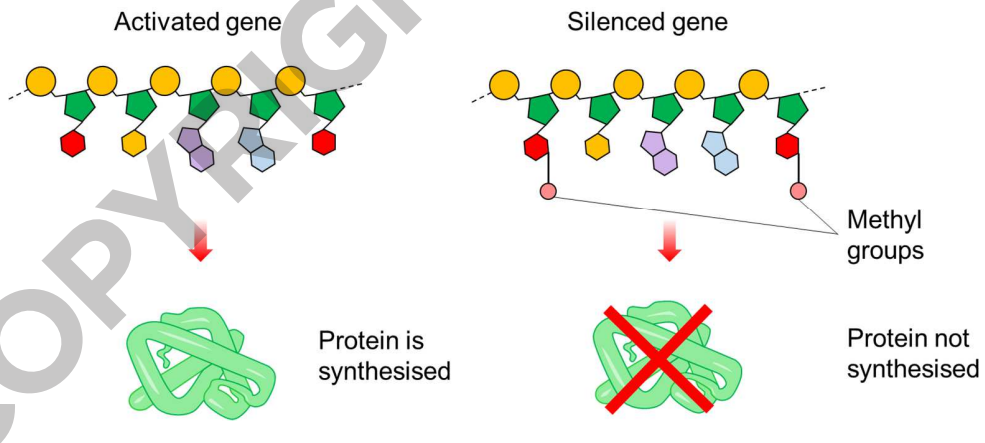


Figure 1.34: Activated and silenced genes.

Chromatin remodelling

Chromatin is a mixture of DNA and protein which makes up eukaryotic chromosomes. DNA molecules are associated with histone proteins in chromatin. DNA molecules are negatively charged due to the presence of phosphate groups in the polynucleotide strands. Histone proteins are positively charged (due to positively charged R groups on amino acids) and this property attracts DNA and permits the formation of tightly-packed **heterochromatin**. Negatively charged acetyl groups neutralise positive charge (on histones) and weaken the bonds between DNA and histones forming loosely-packed **euchromatin** (Figure 1.35).

Question 17

Honeybee (*Apis mellifera*) females occur in two castes: a reproductive queen and workers.

Queen Worker

(a) Worker bees and reproductive queens have the same genotype but different phenotypes.

Explain the difference in phenotype of the queen and worker bees.

(2 marks) **KA2**

(b) Caste is regulated by nutritional factors during the development of honeybee larvae.

Evidence suggests that larvae fed a high concentration of royal jelly will develop into queens.

Ingestion of royal jelly initiates a change in gene expression that results in the development of a queen.

Scientific evidence suggests that this phenomenon is mediated by an epigenetic modification known as DNA methylation.

(1) Identify the nucleotide base in DNA that is affected by DNA methylation.

(1 mark) **KA1**

(2) Enzymes named DNA methyltransferases (DNMTs) add methyl groups to DNA.

Evidence has suggested that components of royal jelly cause silencing of the genes that code for the synthesis of DNMTs.

Explain how silencing genes that code for DNMTs may initiate the development of female reproductive organs in queen bees.

(3 marks) **KA2**

The detector converts the light into an electric cutrrent that is analysed by computer software. The software produces a graph of the data received from a DNA sequencing machine. The graph is called an **electropherogram** (Figure 1.53).

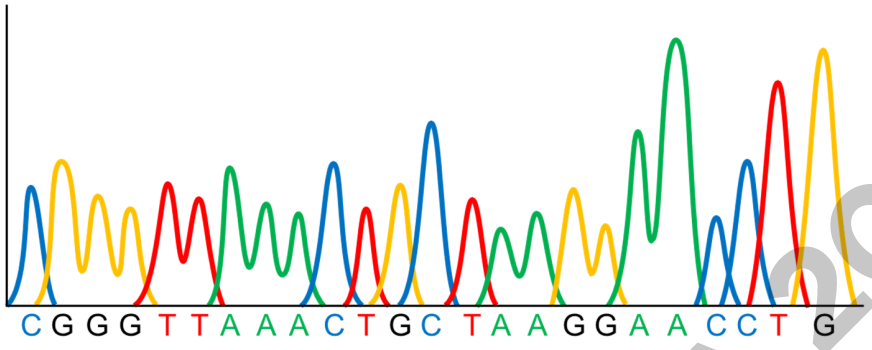


Figure 1.53: Electropherogram

Each peak in an electropherogram represents one of the four DNA nucleotides. The height of each peak is represents the amount of light absorbed and emitted by the fluorescent molecule attached to the ddNTP at the ends of a DNA fragment. The order of the peaks represents the nucleotide sequence of the target DNA molecule.

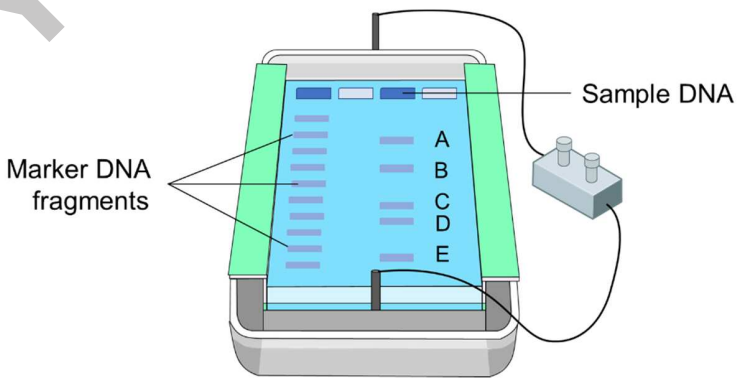
Question 26

Gel electrophoresis is an analytical technique used to separate fragments of DNA in a sample.

(a) State the property of DNA that causes separation of the fragments in gel electrophoresis.

_____ (1 mark) **KA1**

(b) The diagram below shows separation of five DNA fragments, labelled A–E on the gel.



(1) State the letter corresponding to the largest DNA fragment in the sample.

_____ (1 mark) **KA1**

(2) State the function of marker DNA fragments.

_____

_____ (1 mark) **KA1**

Question 28

The koala (*Phascolarctos cinereus*) is a vulnerable species in Queensland and NSW.

Conservation scientists harmlessly extract DNA from koalas in the wild for the purposes of developing a DNA profile.

(a) DNA can be obtained from koala faeces.

State why DNA can be obtained from faeces.

(1 mark) **KA2**

(b) State why PCR is used on the DNA obtained from koala faeces.

(1 mark) **KA1**

(c) Koala faeces contain DNA from eucalypts and bacteria.

Explain why PCR has no effect on DNA from eucalypts or bacteria.

(2 marks) **KA2**

(d) DNA obtained by PCR is used to prepare a DNA profile for a koala.

State two ways that DNA profiles can be used to support both individuals and populations of koalas in Queensland and NSW.

(2 marks) **KA2**

Isolating the target gene

The gene of interest (target gene) is removed from the genome of an organism using **restriction enzymes.** Restriction enzymes cut the sugar phosphate backbone of both polynucleotide strands at specific locations called **restriction sites** on the DNA molecule.

Some restriction enzymes cut straight across the DNA molecule whereas others cut DNA in an offset way. Restriction enzymes that cut straight across the DNA create **blunt ends** (no exposed bases) whereas enzymes that produce an offset cut create **sticky ends** (exposed bases) (Figure 1.66).

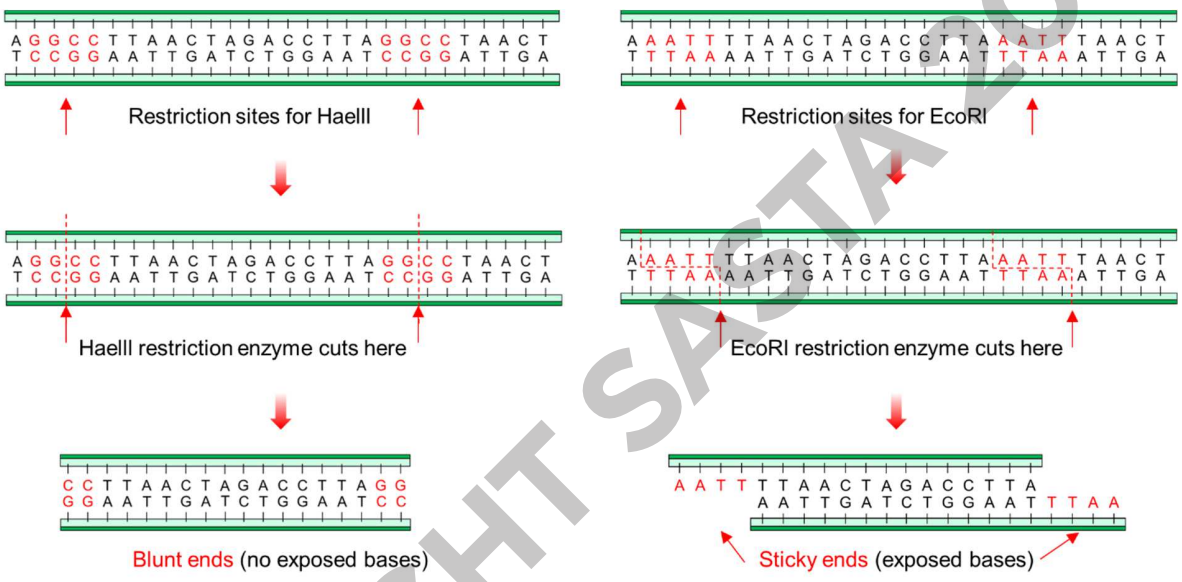


Figure 1.66: Restriction enzymes remove genes from DNA.

The genome of the organism is sequenced to identify restriction sites that are located either side of the target gene. The same restriction enzyme cuts the DNA molecule at both restriction sites which separates the target gene from the genome of the organism (Figure 1.67).

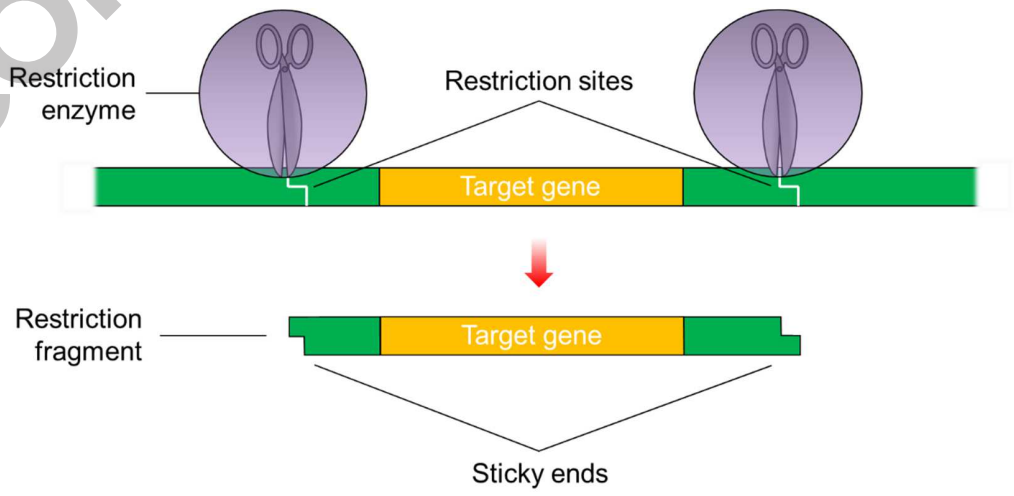


Figure 1.67: Removal of target gene from the genome of an organism.

New technologies, such as CRISPR, can be used to edit and/or transfer genes.

- Discuss the benefits and limitations of the design and manufacture of specific proteins, including endonucleases such as CAS proteins used in CRISPR technology.

CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) is a naturally occurring defence system that bacteria use against viruses that invade them. CRISPR provides bacteria with resistance to viruses called bacteriophages by recognising and destroying viral DNA that has been encountered before.

CRISPR is a length of DNA that is found naturally in the genomes of bacteria in a region called the **CRISPR array**. CRISPR DNA is composed of one short repeating sequence of DNA nucleotides (Figure 1.77).

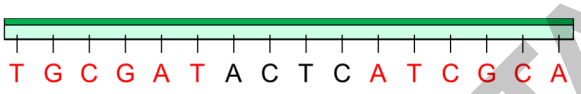


Figure 1.77: Nucleotide sequence found in CRISPR array.

Nucleotides positioned at the ends of each half of the sequence are complementary to each other. This property allows the DNA to fold into a **hairpin structure** (Figure 1.78).

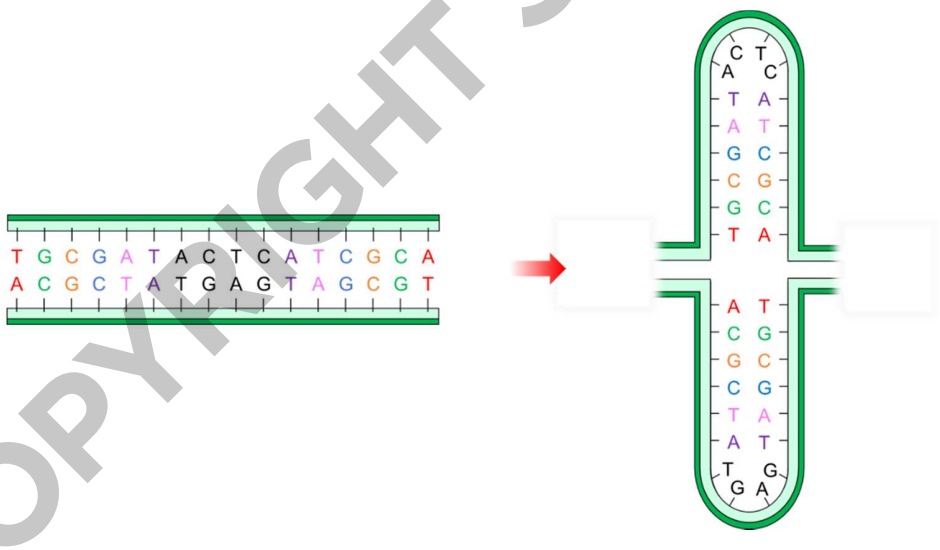


Figure 1.78: Hairpin structure formed by palindromic sequence of DNA in a CRISPR array

The short palindromic repeat sequences are separated by **spacers**. Spacers are short lengths of DNA with sequences that match the DNA sequences found in viruses that attack bacteria. Bacteria incorporate viral DNA (spacers) into the genome to keep record of an infection and to defend against repeat infection. Viral DNA is cut and inserted into the bacterial genome by **Cas proteins** (CRISPR associated proteins).

Cas proteins

Cas proteins are enzymes (nucleases) that break down nucleic acids such as DNA and RNA. Cas proteins are used to cut and paste viral DNA into the CRISPR array to create a new spacer, as well as breaking down invading viruses using information from the spacer.

CRISPR/Cas in Biotechnology

The CRISPR/Cas system is becoming a widely used tool in genetic engineering given the ability of the system to insert or remove any sequence of DNA from the genome of an organism. The most widely used system is **CRISPR/Cas9**.

Cas9 (CRISPR associated protein 9) can cut any target sequence of DNA from the genome of an organism when paired with a synthetic **guide RNA** (gRNA) molecule. The gRNA molecule is synthesised to have a complementary base sequence to the target DNA sequence in the genome of the target organism. The gRNA molecule bonds with the target DNA sequence through complementary base pairing and Cas9 cuts the sugar-phosphate backbone of the DNA at specific locations (Figure 1.79).

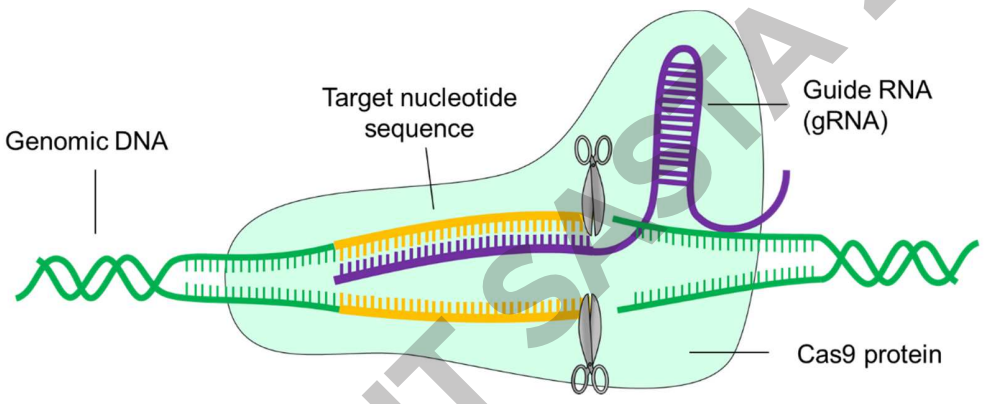


Figure 1.79: Cas9/gRNA complex cuts the target nucleotide sequence.

The genome of a host is edited by then inserting or removing DNA nucleotide sequences.

Benefits and limitations of CRISPR/Cas

CRISPR/Cas is a new technology with enormous potential for selectively editing the genomes of host organisms. Some benefits and limitations of CRISPR are identified in the table below.

Benefit	Limitation
Genomes can be edited more rapidly than in conventional techniques. Multiple genes can be edited simultaneously in the host genome.	Mutations in the target nucleotide sequence of the genome reduces the effectiveness of the Cas9/gRNA complex.
Inexpensive technology (far cheaper than conventional methods of gene editing).	Cuts made by Cas9 can be repaired by enzymes before the genome can be edited.
Gene editing is highly specific and accurate as the Cas9/gRNA complex identifies target nucleotide sequences with high specificity.	Unwanted (off-target) mutations can occur if the target nucleotide sequence for the gRNA appears at multiple sites in the genome.
The gRNA sequence of the Cas9/gRNA complex can be altered to be complementary to any nucleotide sequence in a genome.	CRISPR/Cas recognises short nucleotide sequences (24-48 bp). Shorter sequences are more likely to occur at multiple sites in the genome causing unwanted cuts.

Question 34

Extended response question.

Credit is given for clear, well-expressed answers that are well organised and relevant to the question.

CRISPR/Cas9 is one of the most important discoveries in biotechnology made in recent years.

The CRISPR/Cas9 system has the potential to carry out genome editing functions.

- Describe the function of both guide RNA (gRNA) and Cas9 protein in the process of genome editing by CRISPR/Cas9.
- Explain how CRISPR/Cas9 systems are used to alleviate genetic disease in animals.
- Explain one possible consequence in using CRISPR/Cas9 systems to alleviate genetic disease in humans.

(15 marks) **KA2**

Review Test 1

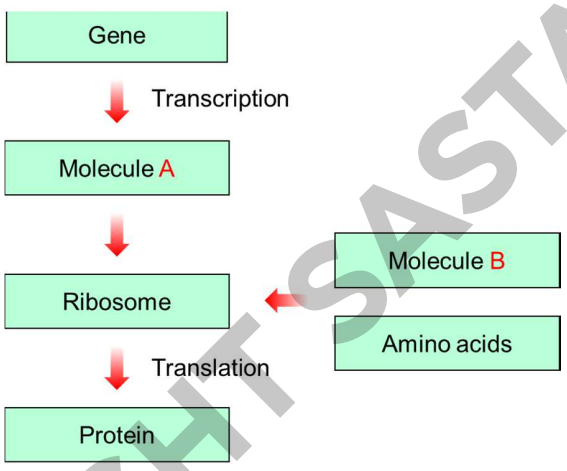
Question 1 (Multiple choice) 1 mark each

(a) A DNA molecule contains 180 000 guanine bases and 220 000 thymine bases.

How many DNA nucleotides does this one molecule of DNA contain?

J. 180 000
K. 220 000
L. 800 000
M. 400 000

(b) The flow chart below shows some stages of protein synthesis.



Which one of the following statements is correct?

J. Molecule A is RNA polymerase/Molecule B is tRNA
K. Molecule A is mRNA/Molecule B is a ribosome
L. Molecule A is RNA polymerase/Molecule B is a ribosome
M. Molecule A is mRNA/Molecule B is tRNA

(c) Some mRNA codons and the amino acids coded for are identified below.

mRNA codon	Amino acid
ACC	Threonine
AUU	Isoleucine
CUU	Leucine
UCC	Serine

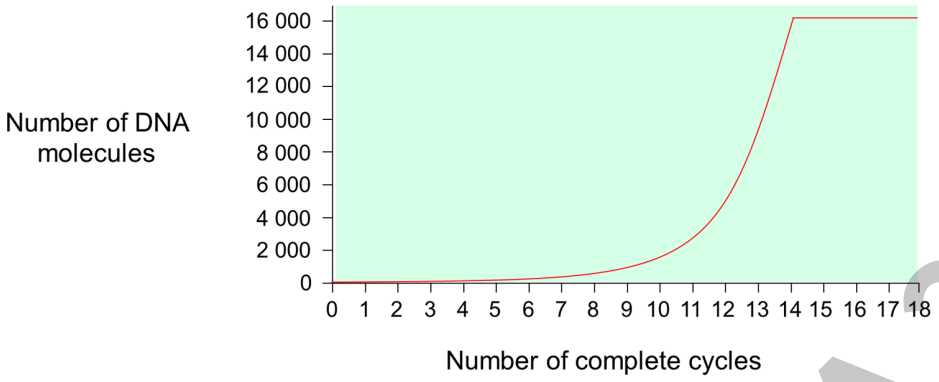
A tRNA molecule has the anticodon AGG

State which amino acid is attached to the tRNA molecule.

J. Threonine
K. Isoleucine
L. Leucine
M. Serine

(i) The graph below shows changes in the number of DNA molecules formed in PCR.

One DNA molecule was used to initiate the reaction.

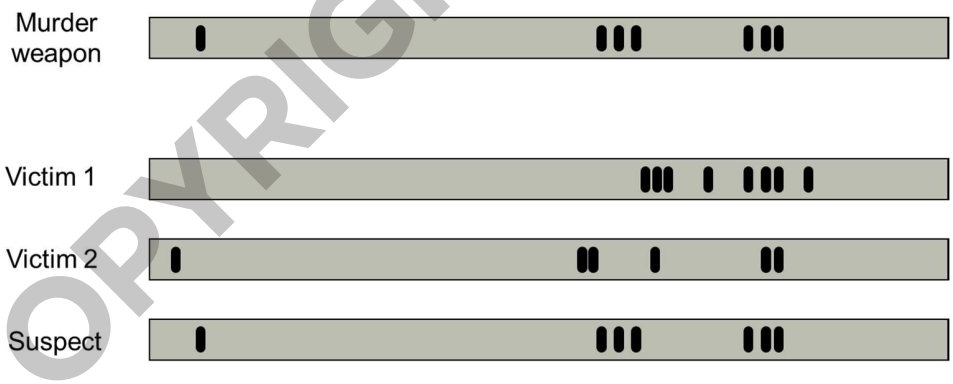


The most likely explanation for the shape of the curve between cycles 14 and 18 is:

J. DNA polymerase has been used up.
K. Primers have been used up.
L. Target DNA has been used up.
M. RNA nucleotides have been used up.

(j) DNA evidence was used in a high-profile murder case in the 1990s.

The DNA profile below was presented as evidence against the suspect.



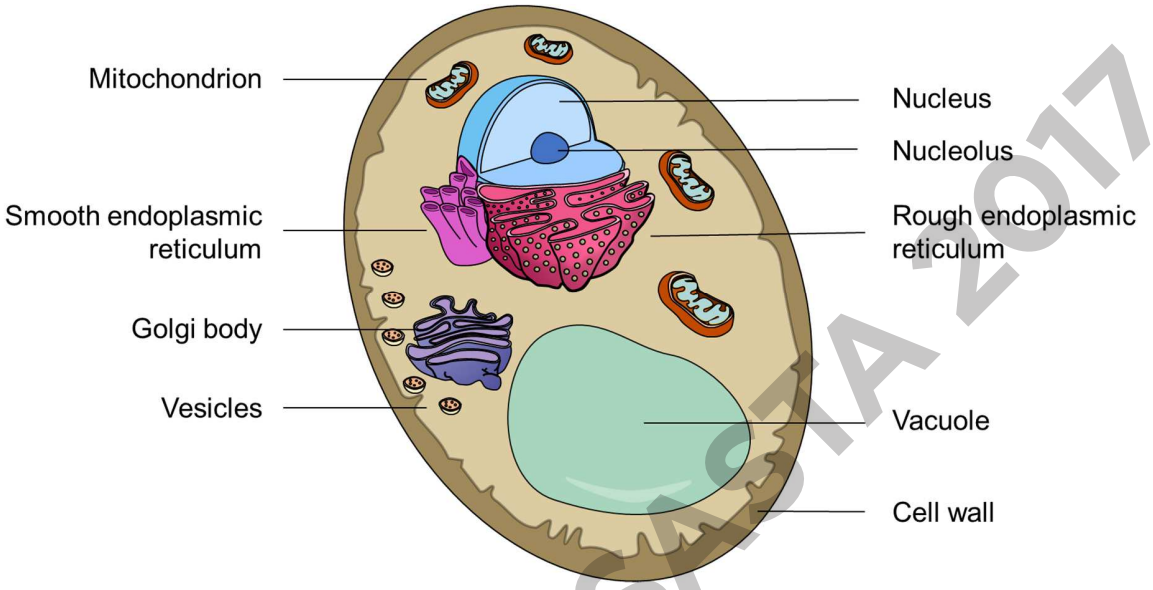
Which one of the following statements is **inaccurate**?

J. DNA on the murder weapon matches the DNA of the suspect.
K. DNA recovered from Victim 1 matches DNA found on the suspect and murder weapon.
L. There is no DNA evidence that the suspect murdered Victim 2.
M. DNA recovered from Victim 2 matches DNA found on the suspect and murder weapon.

Question 38

Saccharomyces cerevisiae is a microorganism used in baking and brewing.

The diagram below shows the typical features of a *Saccharomyces cerevisiae*.



(a) State and explain whether *Saccharomyces cerevisiae* is a prokaryotic or eukaryotic organism.

_____

_____

_____ (2 marks) **KA4**

(b) *Saccharomyces cerevisiae* generates ATP through aerobic and anaerobic respiration.

The two principal respiration reactions occurring in *Saccharomyces cerevisiae* are summarised in the table below.

Reaction	Occurs when:	Products
Alcohol fermentation	Glucose concentration is high	Ethanol and carbon dioxide
Aerobic respiration	Glucose concentration is low	Carbon dioxide and water

(1) Write an equation for alcohol fermentation in *Saccharomyces cerevisiae*.

_____ (2 marks) **KA4**

(2) Two molecules of ATP are synthesised when glucose is converted to ethanol in alcohol fermentation.

Write an equation to show the synthesis of ATP.

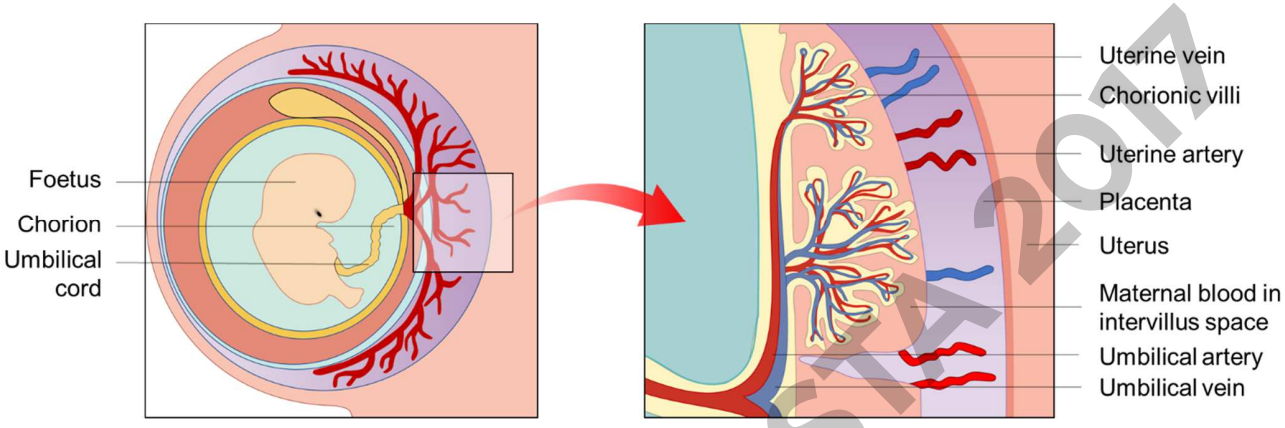
_____ (2 marks) **KA4**

Question 40

The placenta is the life support system of a mammalian fetus growing in a uterus.

Placenta enables the diffusion of important materials from maternal blood into fetal blood.

A labelled diagram of a foetus and its placenta is given below.



(a) Write an equation to show a foetus uses oxygen for growth.

_____ (2 marks) **KA4**

(b) As development continues, the outer surface of the placenta (chorion) becomes folded into finger-shaped chorionic villi.

The cell surface membranes of the chorionic epithelia are folded into microvilli.

State how these features support the growth of a foetus during pregnancy.

_____

_____

_____

_____ (2 marks) **KA2**

(c) The umbilical artery transports blood that is low in oxygen to the placenta.

State how this property supports the diffusion of oxygen into capillaries in the chorionic villi.

_____

_____ (1 marks) **KA2**

(d) Waste materials produced by a foetus are exchanged with maternal blood across the placenta.

Name two waste materials produced by a foetus during growth.

_____

_____ (2 marks) **KA1**

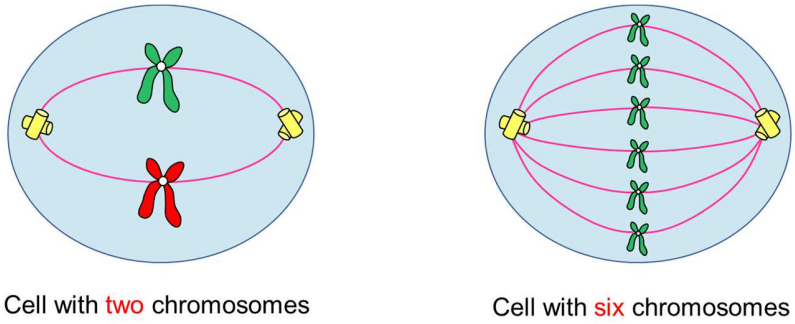


Figure 2.38: Spindle fibres attach to centromeres during metaphase.

Anaphase

The centromeres of the replicated chromosomes are broken down and the sister chromatids are pulled to opposite poles (ends) of the cell by contracting spindle fibres. The parent cell begins to elongate in preparation for cytokinesis (Figure 2.39).

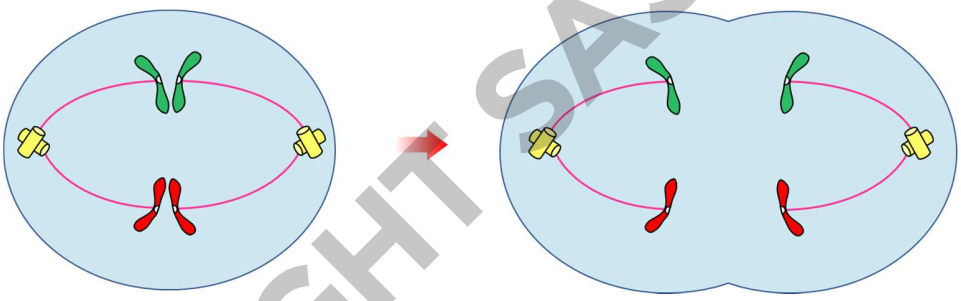


Figure 2.39: Sister chromatids pulled towards opposite ends of the cell during anaphase.

Telophase

Nuclear membranes are assembled around the sets of chromosomes in each of the dividing cells, and the nucleoli reappear. Chromosomes decondense and are no longer visible with an optical microscope (Figure 2.40).

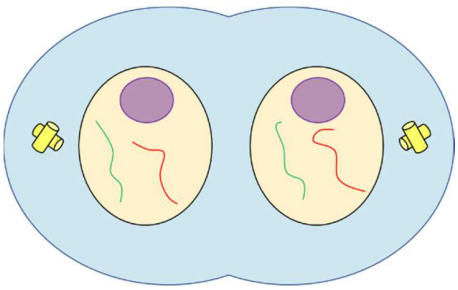


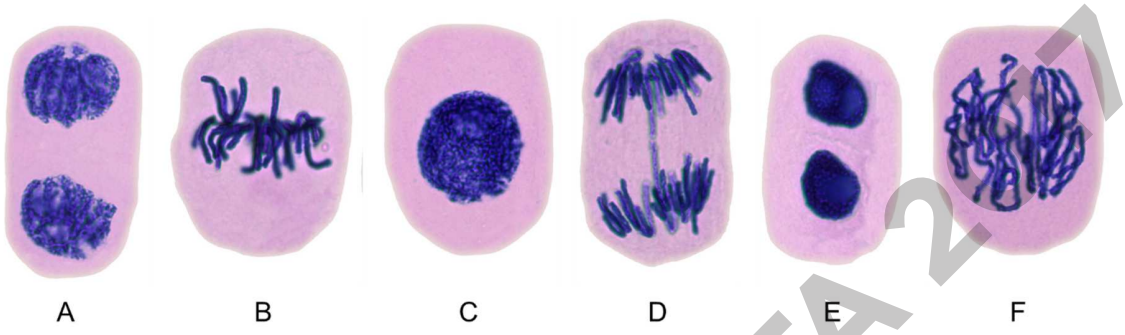
Figure 2.40: Nuclear membranes and nucleoli are reformed in telophase.

Telophase is the final stage of mitosis (division of the nucleus). The second stage of cell division, called cytokinesis, generally begins once the two daughter nuclei are formed in telophase.

Question 49

The diagram below is a light micrograph of root tip cells from an onion (*Allium cepa*) undergoing mitosis.

The stages of mitosis have been purposely disorganised.



(a) Two of the images show events occurring in early prophase and late prophase respectively.

State the image that shows events in early prophase, and give a reason for your answer.

Diagram: _____

_____

_____

State the image that shows events in late prophase, and give a reason for your answer.

Diagram: _____

_____

_____ (4 marks) **KA4**

(b) Diagrams A and E show events that occur in telophase.

Describe the events occurring in diagrams A and E.

_____

_____

_____

_____ (2 marks) **KA4**

(c) The parent cell contains 16 chromosomes.

State the number of chromosomes in the nuclei of both daughter cells immediately after cell division has occurred.

_____ (1 mark) **KA1**

(d) State one difference between mitosis in plants and animals.

_____ (1 mark) **KA1**

Cells that undergo in meiosis in humans are called **spermatocytes** (male) and **oocytes** (female). Spermatocytes are in the male testes and oocytes are in the female ovaries.

Meiosis occurs in two stages called Meiosis I and Meiosis II. Both Meiosis I and II consist of four separate phases; prophase, metaphase, anaphase, and telophase. Prophase I begins after the conclusion of DNA replication.

Prophase I

DNA replication produces replicated chromosomes. The replicated chromosomes condense and the nuclear membrane is broken down at the start of prophase I (Figure 2.47).

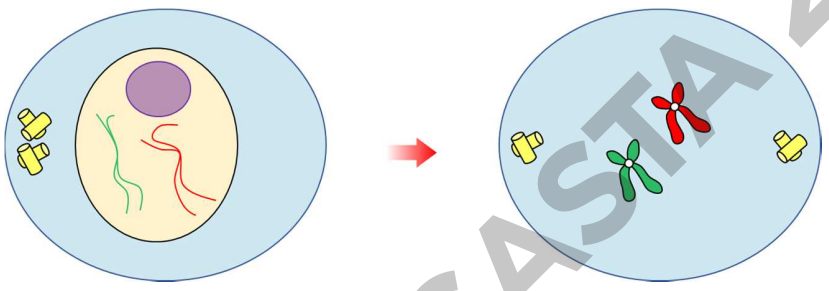


Figure 2.47: Prophase I (meiosis)

Homologous chromosomes then pair up and exchange DNA in a process called **crossing over**. Crossing over involves the exchange of DNA between the sister chromatids of the maternal and paternal chromosome. Chromatids on the maternal chromosome cross over with chromatids on the paternal chromosome at points of contact called **chiasmata** (singular; **chiasma**) (Figure 2.48).

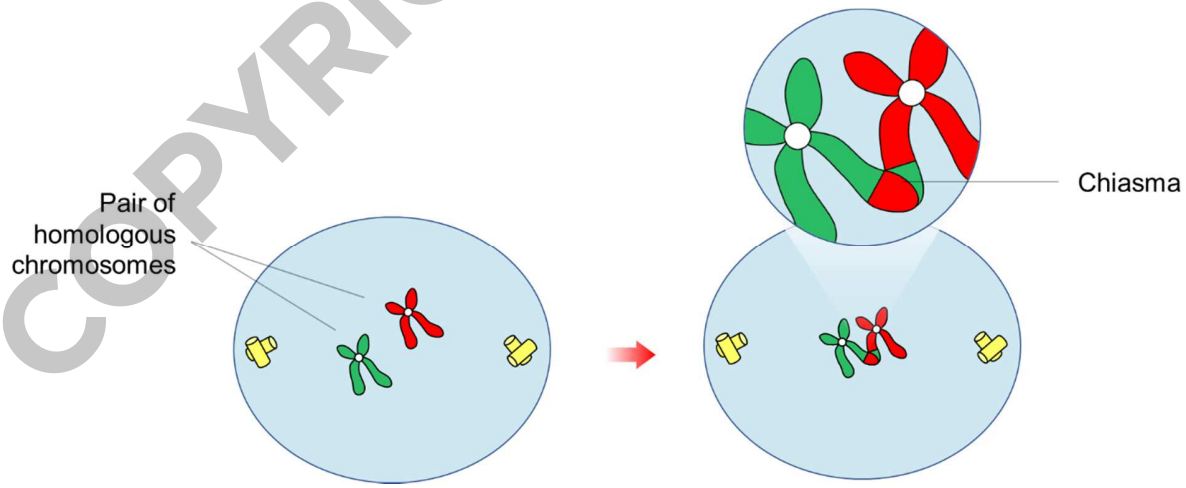


Figure 2.48: Single crossing over event during prophase I (meiosis)

Crossing over between a pair of homologous chromosomes produces four chromatids that are genetically unique. The new combinations of DNA created during crossover are a source of genetic variation in gametes.

The independent assortment of chromosomes introduces genetic variation in the gametes formed in meiosis. The haploid daughter cells have different combinations of chromosomes due to crossing over and independent assortment during metaphase (Figure 2.59).

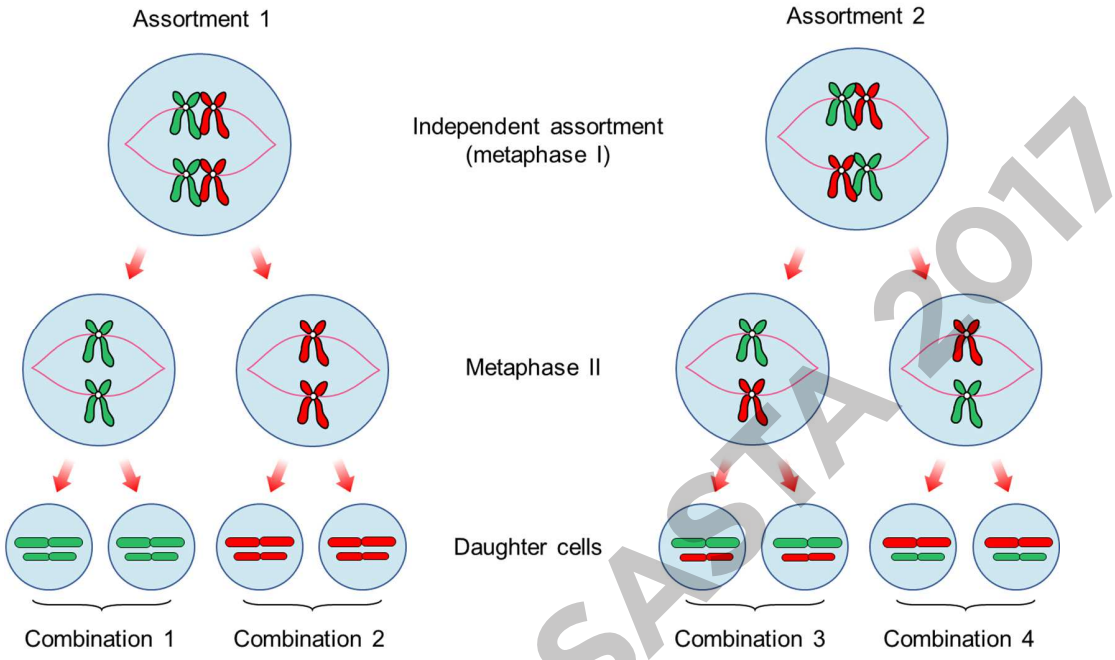


Figure 2.59: Independent assortment during metaphase

Fertilisation

Fertilisation is the event that initiates the development of a new organism in animals and plants. Fertilisation involves the fusion of the male and female gametes (haploid) which produces the first cell in the new organism (zygote). The zygote is a diploid cell given that its nucleus was formed in the fusion of two haploid nuclei. The diploid number of an organism is restored in the zygote through the fusion of haploid male and haploid female gametes during fertilisation

Human fertilisation involves the fusion of sperm and egg. The nuclei of sperm and egg each contains 23 chromosomes. Fusion of the sperm and egg during fertilisation produces a zygote with 46 chromosomes (Figure 2.60).

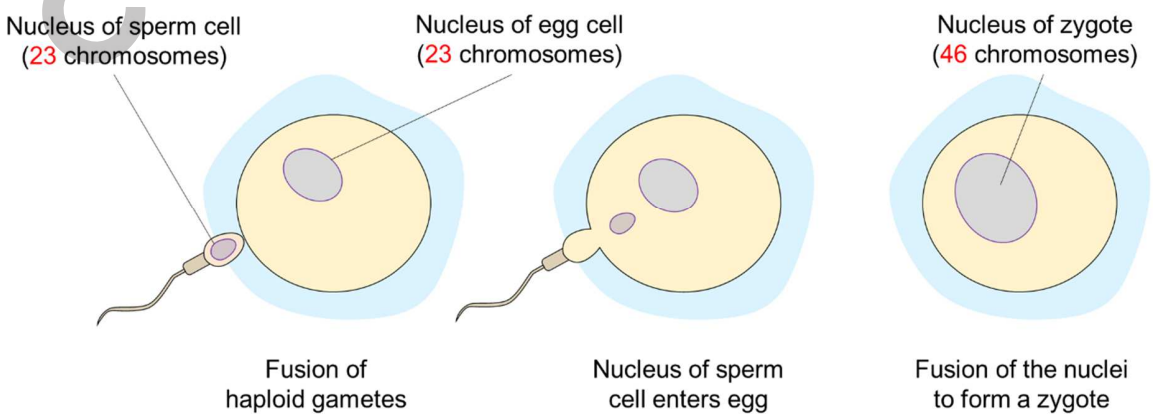


Figure 2.60: Human fertilisation.

Responding to stimuli

Sensory receptors are specialised cells that detect changes in the internal and external environment of an organism. Most sensory receptors are sensitive to one type of stimulus. Sensory receptors are located in sensory organs such as the eyes, skin, mouth and ears. The process by which an organism responds to sensory stimuli in its environment is described by the stimulus-response model.

1. Sensory receptors detect a stimulus.
2. A nerve impulse is transmitted along sensory neurons to the central nervous system (CNS).
3. The information is processed and a response is coordinated by the central nervous system.
4. A nerve impulse is transmitted along motor neurons from the CNS to effectors.
5. Effectors produce the desired response to a stimulus.

Example:

Figure 3.13 describes the response of a thirsty person noticing a drink of water.

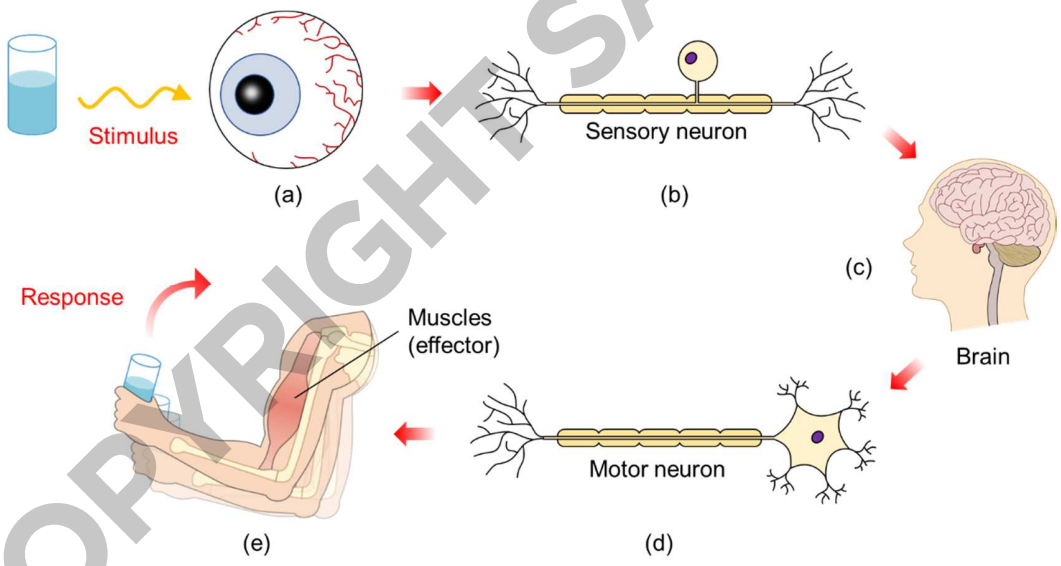


Figure 3.13: Response of a thirsty person noticing a drink of water.

(a)	Light reflects off the drink of water and enters the person's eyes. Sensory receptors in the eyes are stimulated by light.
(b)	An electrical impulse is transmitted along sensory neurons from sensory receptors in the eye to the brain.
(c)	The information is interpreted by the brain which then coordinates a response to the visual stimulus.
(d)	A nerve impulse is transmitted along motor neurons from the brain to muscles (effector) in the person's arm.
(e)	The person uses their muscles to pick up the drink of water and raise it to their mouth.

Synapse

Nerve impulses are transmitted between neurons or between neurons and effectors at junctions called **synapses**. Figure 3.14 shows the structure of a synapse between neurons.

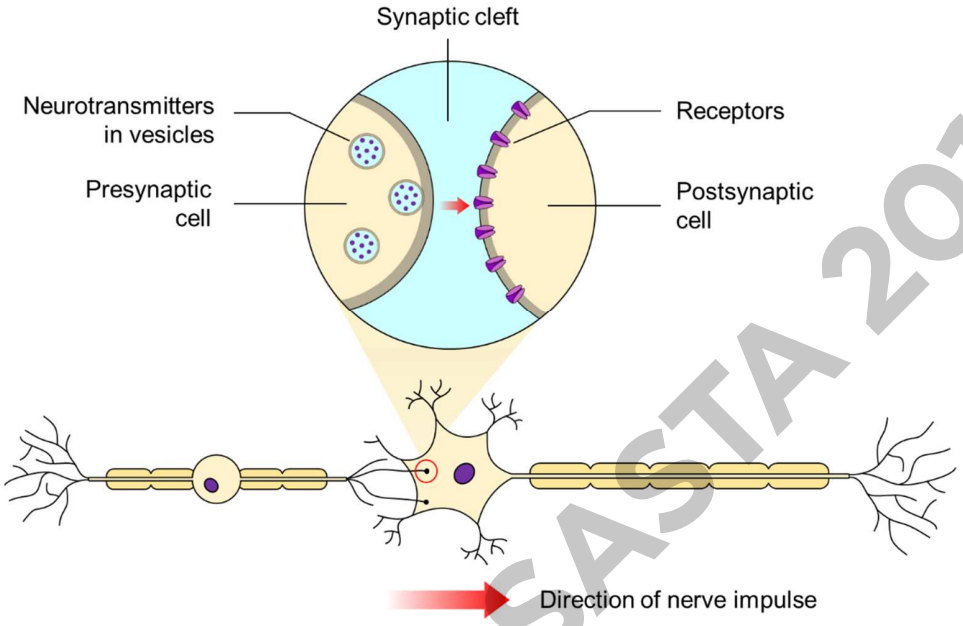


Figure 3.14: Structure of a synapse between neurons.

Neurotransmitters

A nerve impulse is transmitted along the axon until it arrives at the axon terminals of the presynaptic cell. The axon terminals of the presynaptic cell contain molecules called **neurotransmitters** that are packaged into vesicles. The arrival of a nerve impulse to the axon terminals can cause exocytosis of neurotransmitter molecules from the presynaptic cell to the **synaptic cleft**. Neurotransmitters diffuse across the synaptic cleft and bond with specific receptors on the postsynaptic membrane. Each neurotransmitter has its own receptor. Bonding of neurotransmitters to receptors initiates a nerve impulse that travels along the axon of the postsynaptic cell (Figure 3.15).

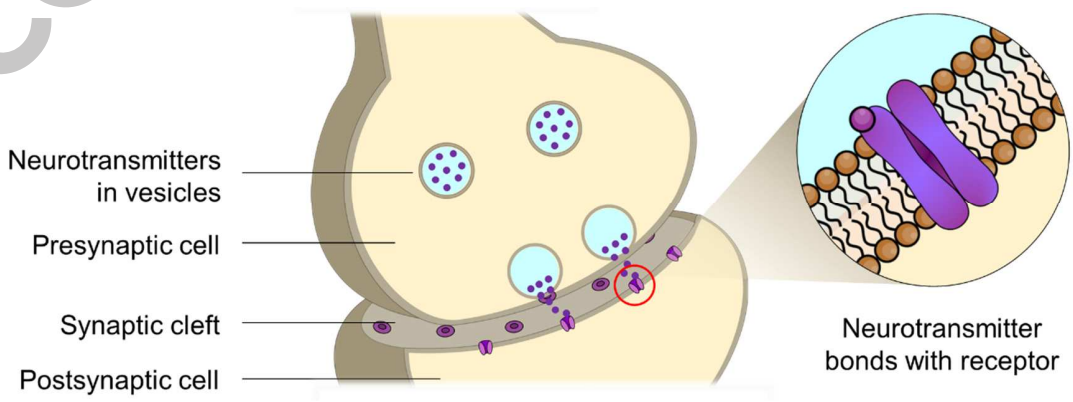


Figure 3.15: Diffusion of neurotransmitters across the synaptic cleft.

Hormones have different actions on target cells. The action of a hormone on a target cell is dependent on the physical properties of the hormone including molecular size and solubility.

Example 1:

Steroid hormones are lipid-soluble and freely diffuse across the membrane of a target cell. Steroid hormones bind with receptors in the cytoplasm or nucleus of the target cell, forming a receptor-hormone complex. This activated complex diffuses the nuclear membrane and binds to DNA. The activated complex initiates the transcription of specific genes in the target cell (Figure 3.18).

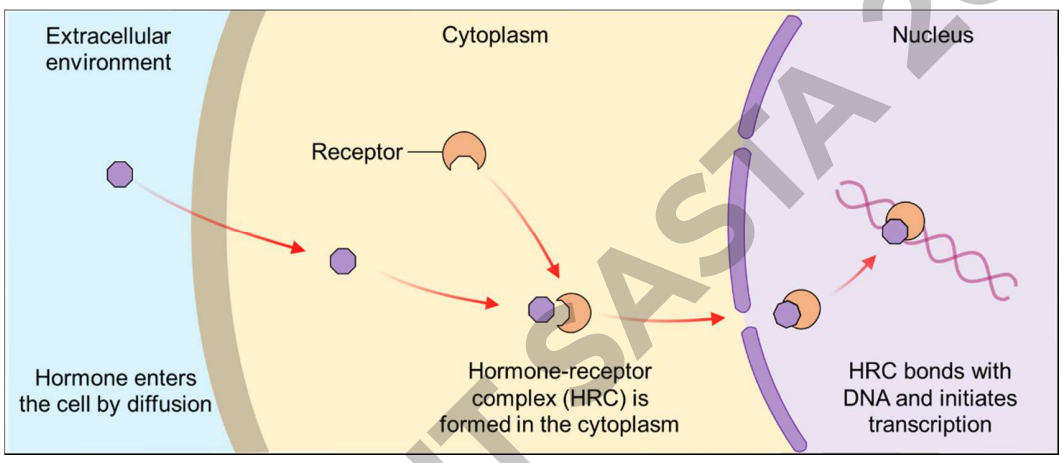


Figure 3.18: Action of a steroid hormone on a target cell.

Example 2:

Peptide hormones are hydrophilic and cannot diffuse across the membrane of target cells. Peptide hormones bind with receptors on the surface of target cells. Binding of the peptide hormone with its receptor activates a series of intracellular (relay) molecules which change the activity of the target cell. Relay molecules change cell activity by activating specific enzymes and by altering gene expression (Figure 3.19).

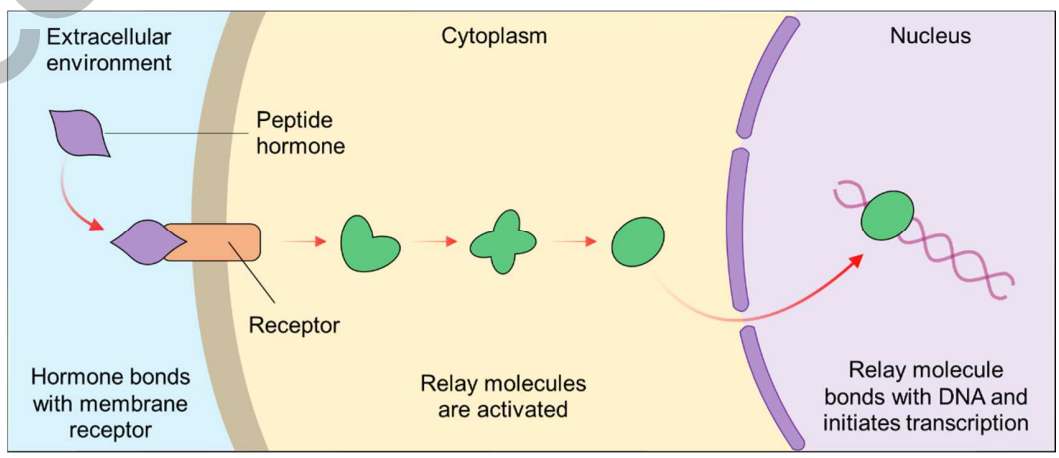


Figure 3.19: Action of a peptide hormone on a target cell.

Hormones can alter the metabolism of target cells, tissues, or organs.

- Describe the action of thyroid-stimulating hormone and thyroxine in metabolism.
- Describe the role of thyroid stimulating hormone in the production of thyroxine.

The rate of metabolism in body cells is regulated by hormones named **thyroid-stimulating hormone** (TSH) and **thyroxine (T_4)**. TSH is synthesised in the pituitary gland (brain) and T_4 is synthesised in the thyroid gland. TSH stimulates the thyroid gland to synthesise T_4. T_4 is converted to a hormone named **triiodothyronine (T_3)** which stimulates metabolism of almost every tissue in the body. T_3 increases heart rate, breathing rate and the rate of cellular respiration.

The secretion of TSH from the pituitary gland, and the subsequent synthesis of T4 in the thyroid gland is regulated by changes in the blood concentration of T_4.

Blood concentration of T4	Response of pituitary gland
Low	Increased secretion of TSH
High	Decreased secretion of TSH

The regulation of thyroxine (T_4) synthesis by thyroid-stimulating hormone (TSH) is an example of a negative feedback loop (Figure 3.24).

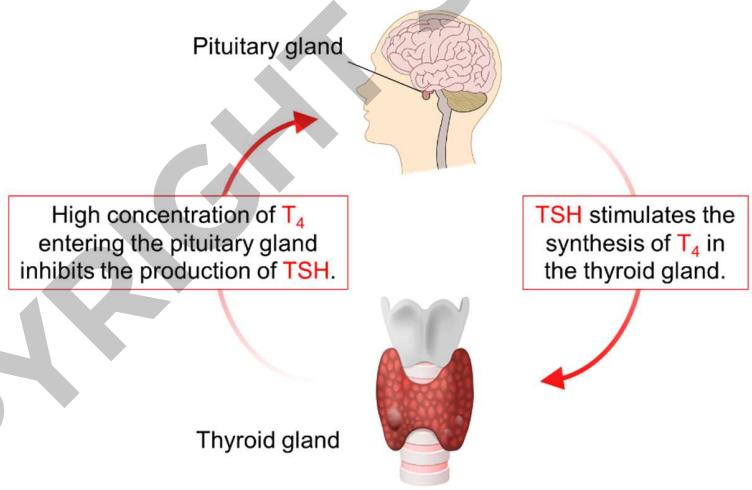


Figure 3.24: Negative feedback loop (T_4 and TSH)

Hypothyroidism and hyperthyroidism

Hypothyroidism and hyperthyroidism are disorders of the endocrine system in which the thyroid gland either synthesises too much or too little thyroid hormones such as T_3 and T_4.

Disorder	Cause	Symptoms
Hypothyroidism	Insufficient production of thyroid hormones by the thyroid gland.	Poor ability to tolerate cold Poor memory and concentration Feeling tired
Hyperthyroidism	Excessive production of thyroid hormones by the thyroid gland.	Poor ability to tolerate heat Rapid heartbeat Irritability and difficulty sleeping

RNA world hypothesis

RNA is a nucleic acid that has both the ability to catalyse metabolic reactions as well as the ability to store and transmit genetic information in cells. The **RNA world hypothesis** suggests that the first cells consisted of an RNA molecule enclosed in a vesicle (Figure 4.04).

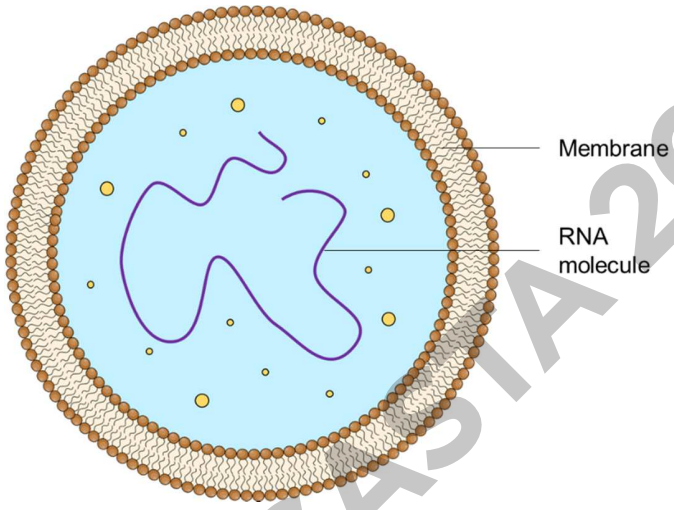


Figure 4.04: Hypothesised structure of the first simple cells.

Several assumptions were made in the development of the RNA world hypothesis.

Assumption	Description
1	Genetic information was stored and transmitted by RNA rather than DNA in the first simple cells.
2	The replication of RNA in the first simple cells followed the same base pairing rules as modern cells (A with U, and C with G).
3	Metabolic reactions were catalysed by RNA molecules rather than enzymes in the first simple cells.

Ribozymes

In the early 1980s, scientists discovered RNA molecules that catalysed metabolic reactions in cells. RNA enzymes, or **ribozymes**, play vital roles in modern cells. The table below identifies two ribozymes that are essential in modern prokaryotes and eukaryotes.

Ribozyme	Description
RNA polymerase	Catalyses the synthesis of RNA molecules from genes during transcription.
Ribosomal RNA	Catalyses the formation of peptide bonds in protein synthesis.

The discovery of ribozymes provided supporting evidence of the RNA world hypothesis by demonstrating that RNA can store genetic material and act as a biological catalyst. It is plausible that ribozymes catalysed metabolic reactions and carried out the process of RNA replication and cell division in the first simple cells.

There is evidence that prokaryotic cells existed before eukaryotic cells.

- Describe this evidence, including fossil evidence.
- Explain how the ancestry of most existing eukaryotic cells probably involved endosymbiotic events.

Fossilised bacteria are the earliest evidence of life on Earth. Fossilised bacteria have been discovered in rock and sediment samples from Australia, Europe, South Africa, and Antarctica.

Figure 4.05 shows fossilised bacteria reported to be 3.5 billion years old.

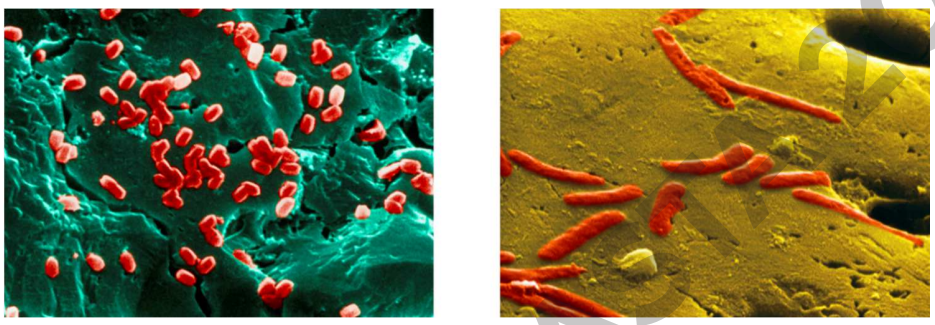


Figure 4.05: Coloured Scanning Electron Micrographs (SEM) of fossilised bacteria.

Stromatolites

Further evidence for early prokaryotes is found in rock-like structures called **stromatolites (Figure 4.06)**.

Figure 4.06: Modern stromatolites (left). Layers of a fossilised stromatolite (right).

Some palaeontologists think stromatolites formed when layers of cyanobacteria trapped sediments and eventually fossilised. Fossilised stromatolites may date from 3.5 billion years ago.

Cyanobacteria are photosynthetic microorganisms that changed the composition of Earth's atmosphere by converting carbon dioxide into oxygen. More complex life forms evolved as the atmospheric concentration of oxygen increased over time.

Phylogenetic tree diagrams represent evolutionary relationships.

- Draw and analyse simple phylogenetic tree diagrams to represent evolutionary relationships.

A **phylogenetic tree** is a diagram showing the inferred evolutionary relationships between individuals and groups of organisms based upon similarities and differences in both genetic and physical features. The organisms displayed in the phylogenetic tree are inferred to have evolved from a common ancestor (Figure 4.11).

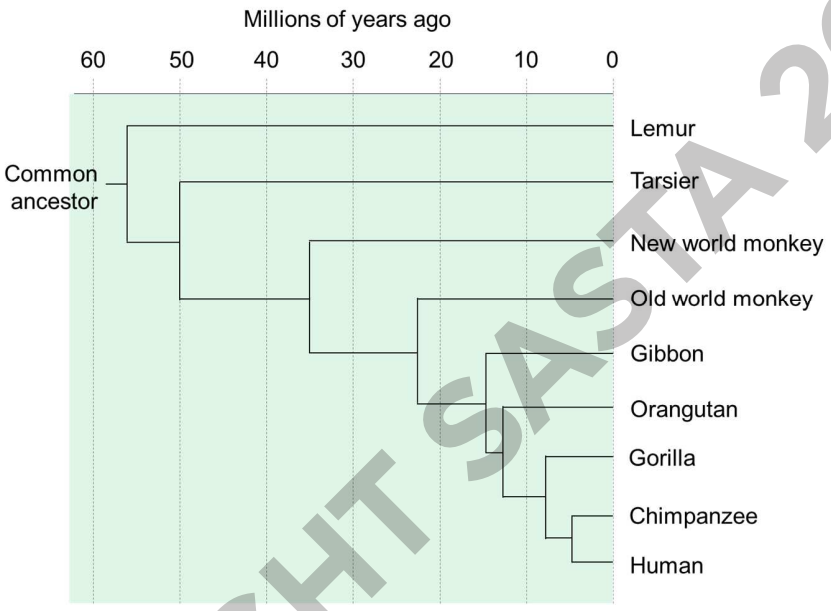


Figure 4.11: Phylogenetic tree showing evolutionary relationships between primates.

Interpreting phylogenetic trees

Phylogenetic trees identify evolutionary relationships between species. The **terminals** of the tree represent species that share a common ancestor. The **nodes** on a phylogenetic tree represent common ancestors of related species. Species that diverge from the same node are called **sister groups.** Members of a sister group are closely related (Figure 4.12).

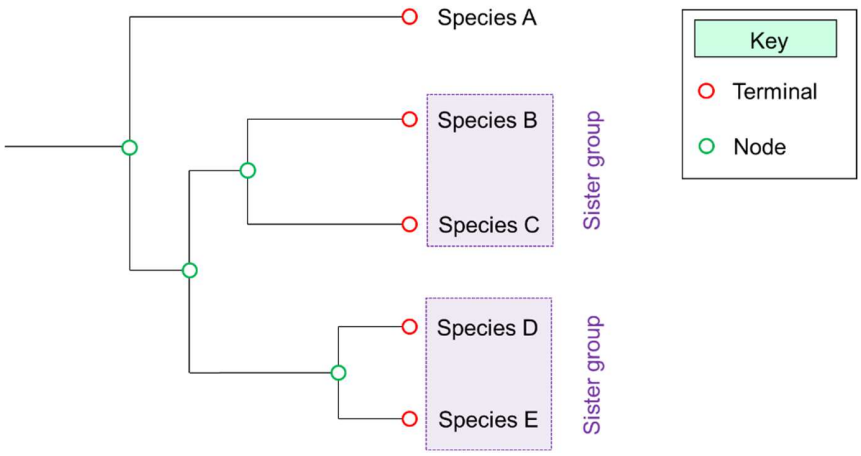


Figure 4.12: Common features of a phylogenetic tree.

Natural selection

Natural selection is the process by which selection pressures result in changes in the gene pool of a population over time. The theory was developed and published independently by Charles Darwin and Alfred Russel Wallace in 1858. Darwin and Wallace proposed that individuals with greater biological fitness are *naturally selected* to survive longer and pass on their genes to the next generation. Individuals with lower biological fitness are less likely to survive selection pressures and pass on their genes.

Example

A population of Snowshoe hares (*Lepus americanus*) contains individuals with brown and white-coloured fur (Figure 4.11).

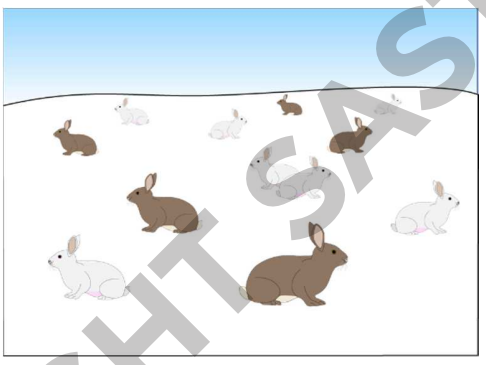


Figure 4.17: Population of Snowshoe hares with brown and white-coloured fur.

During periods of heavy snowfall, the hares with white-coloured fur are better camouflaged than hares with brown-coloured fur. Hares with brown-coloured fur are more likely to suffer predation from animals in higher trophic levels (Figure 4.18).

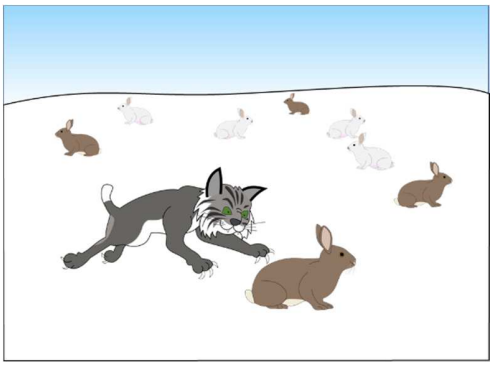


Figure 4.18: Predation of snowshoe hares with brown-coloured fur.

Snowshoe hares with white-coloured fur are more likely to survive predation (selection pressure) during periods of heavy snowfall. In this example, white-coloured snowshoe hares have greater biological fitness and are naturally selected to survive longer and pass on favourable genes to offspring.

Question 95

Staphylococcus aureus is a species of bacteria that infects humans.

Infection with *Staphylococcus aureus* is commonly treated with antibiotics including methicillin.

Individual bacteria in a population of *Staphylococcus aureus* may have a mutation in a gene called *mecA* which codes for a protein that facilities attachment of antibiotics to a bacterium.

(a) Describe how mutation in *mecA* increases the survival rate of *Staphylococcus aureus* in the human body.

(2 marks) **KA3**

(b) Individuals that have the mutation in the *mecA* gene are known as *methicillin-resistant Staphylococcus aureus* (MRSA).

There has been an increase in the population of MRSA due to natural selection in the past 30 years.

The major selection pressure has been the overuse of methicillin and other antibiotics by humans.

(1) Explain the role of natural selection in changing the gene pool of *Staphylococcus aureus.*

(3 marks) **KA3**

(2) State one human intervention that can minimise the evolution of MRSA by natural selection.

(1 mark) **KA3**

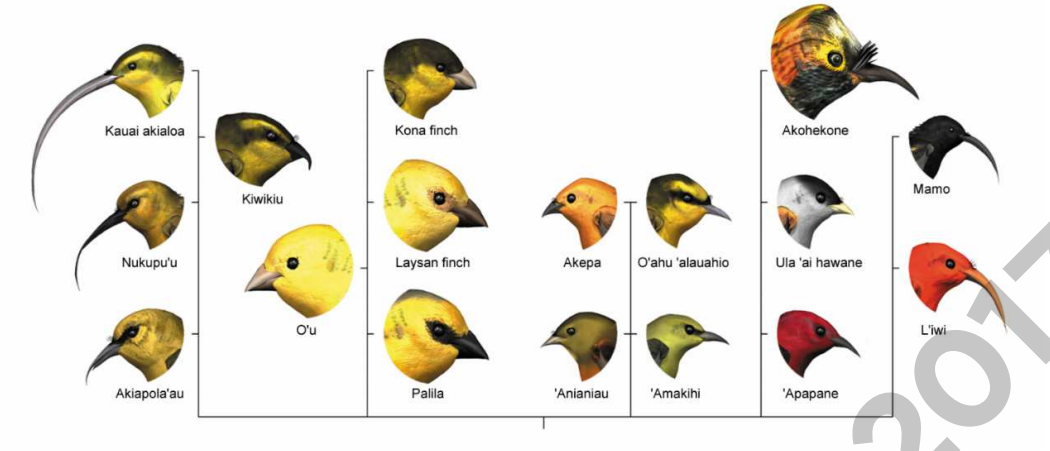


Figure 4.24: Hawaiian honeycreepers

Sympatric speciation

Sympatric speciation is the result of reproductive isolation between two populations in the absence of any physical barrier that prevents gene flow between populations. Some factors that lead to sympatric speciation are identified below.

Isolation mechanism	Description
Ecological	The two populations live in different habitats and are unlikely to mate which prevents gene flow.
Behavioural	A change in courtship behaviour prevents successful mating between populations.
Temporal	The two populations may become fertile or mate at different times of the year which prevents breeding.

Example

Killer whales (*Orcinus orca*) are found in distinct populations called **pods** (Figure 4.25).

Figure 4.25: Pod of killer whales in the Pacific Ocean.

The pods are not separated by any physical barrier but variations in habitat and diet results have resulted in significant genetic diversity between populations in the North Pacific, Atlantic, and Antarctic oceans over the past 10 000 years. Some evolutionary biologists believe that in time, genetically diverse populations of killer whales will be formally described as separate species (sympatric speciation).

Similar selection pressures in different environments may lead to convergent evolution.

- Recognise and give examples of convergent evolution.

Convergent evolution is the process whereby unrelated species independently evolve similar structural, biochemical or behavioural characteristics due to similar selection pressures in their respective environments. Structures that result from convergent evolution are called **analogous structures.**

Example

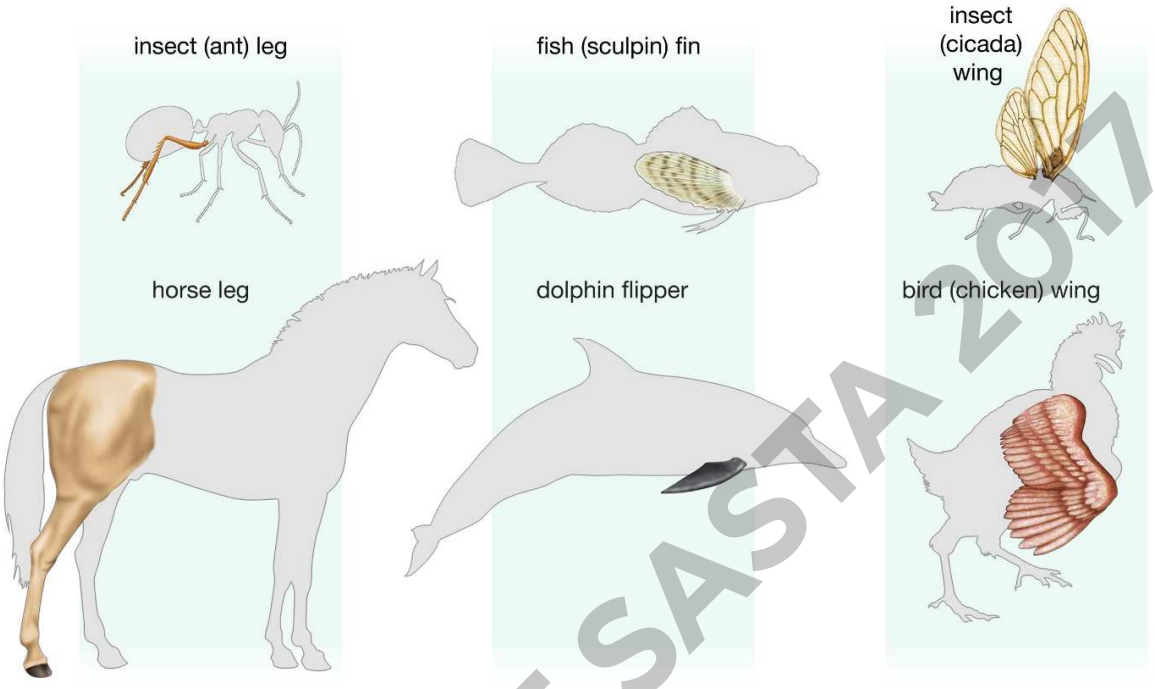
The wings of birds and bats both serve the same function (flight) and are similar in structure, but each evolved independently. Differences in wing structure suggest that the wings of birds and bats were not inherited from a common ancestor. Bird wings consist of feathers extending along the arm, whereas bat wings consist of flaps of skin that are stretched between the bones of the fingers and forearm (Figure 4.26).

Figure 4.26: Analogous wing structures in birds (top) and bats (bottom).

The wings of birds and bats are examples of analogous structures as they evolved from different ancestors for the same function. Birds and bats share similar ecological niches and have faced similar selection pressures in their history which has led to the evolution of analogous structures.

Question 103

The diagram below shows pairings of organisms that have analogous structures.



(a) Define the term analogous structure using the example of the insect and horse leg.

(2 marks) **KA2**

(b) State the primary function of the analogous structure in insects and birds.

(1 mark) **KA2**

(c) Fish and dolphins share an ecological niche but are not very closely related species.

Suggest a reason why both fish and dolphins evolved fins (analogous structures).

(2 marks) **KA2**

Homologous structures

Structures or features that are similar because of common ancestry are called **homologous structures**. Homologous structures are evidence of adaptive radiation as the structures have evolved from a common ancestor. A common example is the arrangement of bones in the forelimb of all mammals (Figure 4.28).

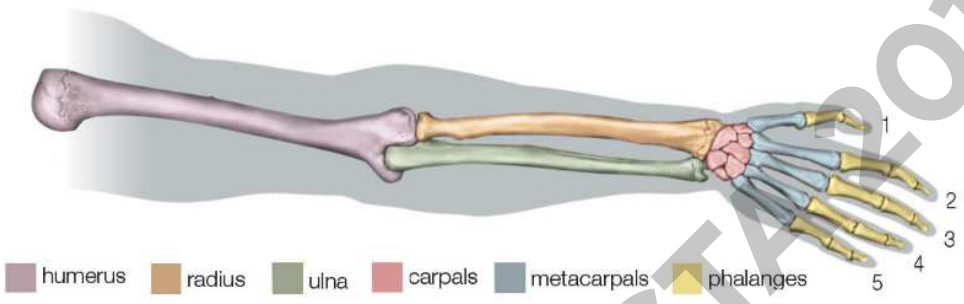
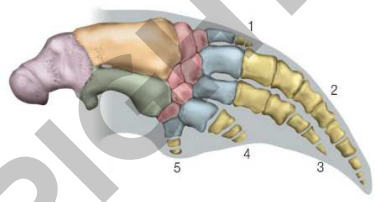
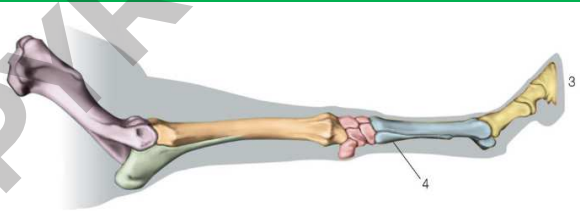
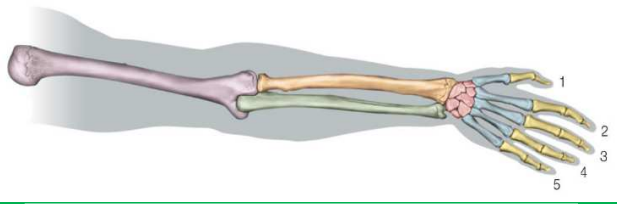
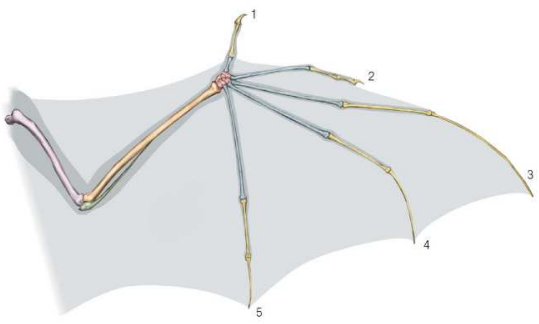


Figure 4.28: The bones of the human forelimb.

The arrangement of bones in the forelimbs of mammals has been modified through evolution to allow the different species to adapt to different ecological niches.

Mammal	Arrangement of bones	Function
Dolphin		Forelimbs are flippers that are adapted for swimming.
Horse		Bones are fused together forming elongated structures that provide a large surface area for leg muscles (enables fast running).
Human		Finger bones and opposable thumbs are adapted for manipulating objects and grasping tools.
Bat		Forelimbs are a wing structure that enables flight over short distances. The first digit is a hook that allows the bat to hang from trees.

Cats were deliberately introduced to Australia in the 19th century to control the population size of rabbits, rats and mice. Feral cats have since caused the extinction of many native Australian species including many ground-dwelling birds and mammals. The black-footed rock wallaby (*Petrogale lateralis*) is an endangered species native to Australia that is at risk of extinction due to predation by feral cats and other introduced species (Figure 4.37).

Figure 4.37: The black-footed rock wallaby

Habitat destruction

Habitat destruction is a process in which a natural habitat is destroyed, and the biodiversity of an ecosystem is reduced. Human activity is the primary cause of habitat destruction. Humans clear land primarily to harvest natural resources and for urbanisation. Habitat destruction is considered the leading cause of species extinction worldwide.

Example

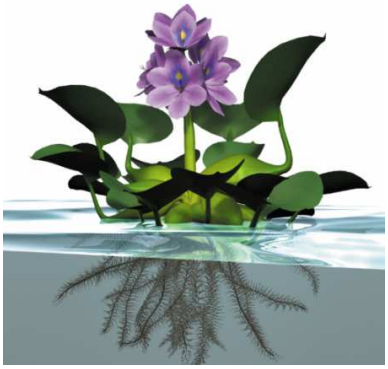
The koala (*Phascolarctos cinereus*) is a marsupial species native to Southern and Eastern Australia.

Figure 4.38: Koala eating eucalyptus leaves.

Australia's koala population faces extinction in some parts of Australia due to increased land clearing for agriculture, urbanisation and commercial logging. These human activities have destroyed the population of native eucalyptus plants (gum trees) that form a major part of the koala's ecological niche. The koala population of New South Wales and Queensland is in serious decline because of habitat destruction, predation by domestic animals and livestock, bushfires and road accidents.

Question 108

The water hyacinth (*Eichhornia crassipes*) is an aquatic plant native to South America.



The water hyacinth was introduced to Australia in the early 1900s as an ornamental plant.

(a) Water hyacinths are classified as an invasive species in Australia.

The rapid growth rate leads to the overgrowth of water hyacinth on the water surface.

Describe how the uncontrolled growth of water hyacinths can lead to the death of aquatic plants and animals.

(4 marks) **KA2**

(b) State one economic consequence of uncontrolled growth of water hyacinth in Australia.

(1 mark) **KA3**

(c) The growth of water hyacinths can be controlled using herbicides such as 2,4-D.

In 2015, the World Health Organisation declared 2,4-D as a potential carcinogen.

State a consequence of Australians using 2,4-D to control the growth of water hyacinths.

(1 mark) **KA3**

(d) The mottled water hyacinth weevil, (*Neochetina eichhorniae*) is an insect species that was introduced from South America by the CSIRO in 1975 to control the growth of water hyacinths in Australia.

(1) Explain how weevils control the growth of water hyacinths.

(2 marks) **KA3**

(2) The lifecycle of the weevil is 90 days.

State a limitation in using weevils to control the growth rate of water hyacinths.

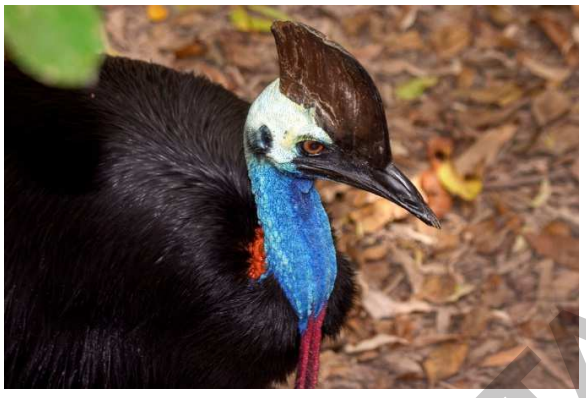
(1 mark) **KA3**

(3) State one other consequence of introducing weevils to control the growth of water hyacinths in Australia.

(1 mark) **KA3**

Question 109

The southern cassowary (*Casuarius casuarius johnsonii*) is a large, flightless bird native to tropical rainforests in far north Queensland.



(a) The southern cassowary spreads the seeds of rainforest trees.

Scientists have identified over 200 different seeds in the droppings of the southern cassowary spread over hectares of rainforest.

(1) Explain the role of the southern cassowary in maintaining species diversity in the rainforest ecosystem.

_____

_____

_____

_____ (2 marks) **KA3**

(2) Many fruits produced by rainforest trees are large in size.

State the importance of the southern cassowary in the rainforest ecosystem.

_____

_____ (1 mark) **KA3**

(b) The habitats of the southern cassowary have been greatly reduced by land clearing.

One reason for land clearing is to allow for urbanisation and expansion of human settlements.

(1) State one other reason why humans clear land.

_____

_____ (1 mark) **KA3**

Solutions: Chapter One			
Question	Part	Author's response	Marks
1	(a)	A: phosphate group	1
		B: sugar	1
		C: base/nucleobase/nucleotide base/nitrogenous base	1
		D: hydrogen bond	1
	(b)	Thymine = 31.2%; DNA has an equal amount of thymine and adenine.	1
		Cytosine = 18.8%; thymine and adenine make up (31.2 x 2) = 62.4% of DNA. Cytosine and guanine must make up the remaining (100−62.4) 37.6%. Cytosine and guanine each make up 37.6 ÷ 2 = 18.8%.	1
		Guanine = 18.8%; DNA has an equal amount of cytosine and guanine.	1
	(c)	**Any one similarity** Both are composed of nucleotides; Both contain adenine, cytosine, and guanine; Both contain a sugar; Both contain phosphate;	1
		Any one difference Sugar in DNA is deoxyribose/sugar in RNA is ribose; DNA is double stranded/RNA is single stranded; DNA contains thymine/RNA contains uracil; DNA is a much longer molecule.	1
2	(a)	J: Adenine	1
		K: cytosine	1
		L: Thymine	1
	(b)	Free DNA nucleotides bind to exposed nucleotides on the DNA template strand via complementary base pairing (adenine with thymine and cytosine with guanine).	1
		Complementary base pairs interact through hydrogen bonds.	1
	(c)	Helicase breaks the weak hydrogen bonds between the bases on the polynucleotide strands of the original DNA molecule.	1
		DNA polymerase joins the sugar and phosphate groups of adjacent (free) nucleotides creating the sugar-phosphate backbone of the newly synthesised polynucleotide strands.	1
3	(a)	The conservative model states that the original double-stranded DNA molecule serves as the complete template for a DNA molecule made from two new strands.	1
		The semiconservative model states that the two strands of the original DNA molecule separate, and each strand serves as a template for a new DNA strand.	1
		The dispersive model states that the original DNA molecule breaks into fragments that serve as templates for new DNA fragments.	1
	(b)	Semi-conservative model.	1
4		The purpose of DNA replication is to synthesise new DNA molecules that will be partitioned into daughter cells during cell division.	2
		An enzyme named helicase breaks the weak hydrogen bonds between the bases on the polynucleotide strands of the original DNA molecule.	2
		Free DNA nucleotides are attracted to the exposed complementary bases on the template strands. Hydrogen bonds are formed between the free nucleotides and the bases on the template strands.	2
		An enzyme named DNA polymerase joins the sugar and phosphate groups of adjacent (free) nucleotides creating the sugar-phosphate backbone of the newly synthesised polynucleotide strands.	2
		Chlormethine forms chemical bonds with guanine bases on opposing polynucleotide strands of the DNA molecule.	2
		Polynucleotide strands do not separate and cannot be replicated which prevents division of cancer cells.	2

Solutions: Test One			
Question	Part	Author's response	Marks
1	(a)	L	1
	(b)	M	1
	(c)	M	1
	(d)	L	1
	(e)	K	1
	(f)	K	1
	(g)	J	1
	(h)	M	1
	(i)	K	1
	(j)	L	1
2	(a)	W: Thymine	1
		X: Adenine	1
		Y: Guanine	1
	(b)	Due to complementary base pairing between adenine/thymine (A/T) and cytosine/guanine (C/G) nucleotides.	1
	(c)	**Either:** Template for a new polynucleotide strand during DNA replication/DNA synthesis/PCR; Provides stability and protection to the coding strand.	1
	(d)	**Any two:** Not all DNA codes for proteins/ exons code for proteins; non-coding DNA / introns present in the molecule; start codons / stop codons present;	1+1
3	(a)	238 x 3 = 714	1
	(b)	Secondary structure is shorter due to folding of the polypeptide chain.	1
	(b)	Gene mutation causes change in the DNA nucelotide base sequence/coding sequence; Mutation causes change in the primary structure of the protein which, in turn, causes a change in the tertiary structire of GFP. Mutations result in GFP folding into a shape that does not support the chromophore ∴ no light is emitted.	1 1 1
	(d)	The shape of the enzyme active site is complementary to the shape of TNT. No other substrate has a shape that is complementary to the active site of the enzyme.	1 1
	(e) (1)	Molecule contains DNA from two different organisms (jellyfish and bacteria).	1
	(e) (2)	Grow the transgenic plants in areas where land mines are likely to be located; Transgenic plants that contain the recombinant DNA will fluoresce in the presence of TNT from nearby landmines; Scientists look for fluorescent plants (at night) as positive identification/detection of TNT.	1 1 1
	(e) (3)	Bacteria can be used to break down TNT in land mines which allows farmers to grow crops on contaminated land again.	1